

SEQUENCE LISTING

<110> Franciso, Joseph
McDonagh, Charlotte

<120> MODIFIED L49-sFv EXHIBITING INCREASED STABILITY AND METHODS OF USE
THEREOF

<130> 9632-082-999

<140> 10/537,143 (National stage of PCT/US02/38414)

<141> 2002-12-02 (371c date)

<160> 23

<170> PatentIn version 3.0

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<211> 753

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(753)

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Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser	
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Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr	
35 40 45	
atg ggt tac ata agc gac agt ggt atc act tac tac aat cca tct ctc	192
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50 55 60	
aaa agt cgc att tcc atc act cga gac aca tcc aag aac caa tac tac	240
Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr	
65 70 75 80	
ctc cag ttg aat ttt gtg act gct gag gac aca gcc aca tat aac tgt	288
Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys	
85 90 95	
gca aga agg act ctg gct act tac tat gct atg gac tac tgg ggt caa	336
Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln	
100 105 110	
gga acc tct gtc acc gtc tcc tca ggc tcg acg tcc ggc tct ggc aaa	384
Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys	
115 120 125	
ccg ggc tct ggc gaa ggc tot acc aag ggc gat ttt gtg atg acc caa	432
Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln	
130 135 140	
act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct	480
Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser	
145 150 155 160	
tgc agg gct agt cag agc ctt gta cac agt aat gga aac acc tat tta	528
Cys Arg Ala Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu	
165 170 175	
cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac	576

His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr		
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Arg	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser		
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Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu		
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gat	ctg	gga	gtt	tat	ttc	tgc	tct	caa	agt	aca	cat	gtt	cct	ccg	acg	720	
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ttc	ggt	gga	ggc	acc	aag	ctg	gaa	atc	aaa	cgg						753	
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Leu	Gln	Leu	Asn	Phe	Val	Thr	Ala	Glu	Asp	Thr	Ala	Thr	Tyr	Asn	Cys		
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Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser		
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Cys	Arg	Ala	Ser	Gln	Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu		
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His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr		
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Arg	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser		
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<220>
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<222> (1)..(1839)

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cag act ctg tcc ctc acc tgt tct gtc act ggc gac tcc atc acc agt	96
Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser	
20 25 30	
ggg tac tgg aac tgg atc cgg aag ttc cca ggg aat aaa ctt gaa tat	144
Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr	
35 40 45	
atg ggt tac ata agc gac agt ggt atc act tac tac aat cca tct ctc	192
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50 55 60	
aaa agt cgc att tcc atc act cga gac aca tcc aag aac caa tac tac	240
Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr	
65 70 75 80	
ctc cag ttg aat ttt gtg act gct gag gac aca gcc aca tat aac tgt	288
Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys	
85 90 95	
gca aga agg act ctg gct act tac tat gct atg gac tac tgg ggt caa	336
Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln	
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gga acc tct gtc acc gtc tcc tca ggc tgc acg tcc ggc tct ggc aaa	384
Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys	
115 120 125	
ccg ggc tct ggc gaa ggc tct acc aag ggc gat ttt gtg atg acc caa	432
Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln	
130 135 140	
act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct	480
Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser	
145 150 155 160	
tgc agg gct agt cag agc ctt gta cac agt aat gga aac acc tat tta	528
Cys Arg Ala Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu	
165 170 175	
cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac	576
His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Ile Tyr	
180 185 190	
aga gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt	624
Arg Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser	
195 200 205	
gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag	672
Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu	
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gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt cct ccg acg	720

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Lys	Gln	Leu	Ala	Glu	Val	Val	Ala	Asn	Thr	Ile	Thr	Pro	Leu	Met	Lys	
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Ala	Gln	Ser	Val	Pro	Gly	Met	Ala	Val	Ala	Val	Ile	Tyr	Gln	Gly	Lys	
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Pro	His	Tyr	Tyr	Thr	Phe	Gly	Lys	Ala	Asp	Ile	Ala	Ala	Asn	Lys	Pro	
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Val	Thr	Pro	Gln	Thr	Leu	Phe	Glu	Leu	Gly	Ser	Ile	Ser	Lys	Thr	Phe	
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Thr	Gly	Val	Leu	Gly	Gly	Asp	Ala	Ile	Ala	Arg	Gly	Glu	Ile	Ser	Leu	
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gac	gat	gcg	gtg	acc	aga	tac	tgg	cca	cag	ctg	acg	ggc	aag	cag	tgg	1056
Asp	Asp	Ala	Val	Thr	Arg	Tyr	Trp	Pro	Gln	Leu	Thr	Gly	Lys	Gln	Trp	
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cag	ggt	att	cgt	atg	ctg	gat	ctc	gcc	acc	tac	acc	gct	ggc	ggc	ctg	1104
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Pro	Leu	Gln	Val	Pro	Asp	Glu	Val	Thr	Asp	Asn	Ala	Ser	Leu	Leu	Arg	
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Phe	Tyr	Gln	Asn	Trp	Gln	Pro	Gln	Trp	Lys	Pro	Gly	Thr	Thr	Arg	Leu	
385					390					395					400	
tac	gcc	aac	gcc	agc	atc	ggt	ctt	ttt	ggt	gcg	ctg	gcg	gtc	aaa	cct	1248
Tyr	Ala	Asn	Ala	Ser	Ile	Gly	Leu	Phe	Gly	Ala	Leu	Ala	Val	Lys	Pro	
				405					410					415		
tct	ggc	atg	ccc	tat	gag	cag	gcc	atg	acg	acg	cgg	gtc	ctt	aag	ccg	1296
Ser	Gly	Met	Pro	Tyr	Glu	Gln	Ala	Met	Thr	Thr	Arg	Val	Leu	Lys	Pro	
			420					425					430			
ctc	aag	ctg	gac	cat	acc	tgg	att	aac	gtg	ccg	aaa	gcg	gaa	gag	gcg	1344
Leu	Lys	Leu	Asp	His	Thr	Trp	Ile	Asn	Val	Pro	Lys	Ala	Glu	Glu	Ala	
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His	Tyr	Ala	Trp	Gly	Tyr	Arg	Asp	Gly	Lys	Ala	Val	Arg	Val	Ser	Pro	
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ggt	atg	ctg	gat	gca	caa	gcc	tat	ggc	gtg	aaa	acc	aac	gtg	cag	gat	1440
Gly	Met	Leu	Asp	Ala	Gln	Ala	Tyr	Gly	Val	Lys	Thr	Asn	Val	Gln	Asp	
465					470					475					480	
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Met	Ala	Asn	Trp	Val	Met	Ala	Asn	Met	Ala	Pro	Glu	Asn	Val	Ala	Asp	
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gcc	tca	ctt	aag	cag	ggc	atc	gcg	ctg	gcg	cag	tcg	cgc	tac	tgg	cgt	1536
Ala	Ser	Leu	Lys	Gln	Gly	Ile	Ala	Leu	Ala	Gln	Ser	Arg	Tyr	Trp	Arg	
			500					505					510			
atc	ggg	tca	atg	tat	cag	ggt	ctg	ggc	tgg	gag	atg	ctc	aac	tgg	ccc	1584
Ile	Gly	Ser	Met	Tyr	Gln	Gly	Leu	Gly	Trp	Glu	Met	Leu	Asn	Trp	Pro	
		515					520					525				
gtg	gag	gcc	aac	acg	gtg	gtc	gag	acg	agt	ttt	ggt	aat	gta	gca	ctg	1632
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Ala	Pro	Leu	Pro	Val	Ala	Glu	Val	Asn	Pro	Pro	Ala	Pro	Pro	Val	Lys	

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Ala Ser Trp Val His	Lys Thr Gly Ser Thr	Gly Gly Phe Gly Ser Tyr					
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gtg gcc ttt att cct	gaa aag cag atc ggt	att gtg atg ctc gcg aat	1776				
Val Ala Phe Ile Pro	Glu Lys Gln Ile Gly	Ile Val Met Leu Ala Asn					
	580	585	590				
aca agc tat ccg aac	ccg gca cgc gtt gag	gcg gca tac cat atc ctc	1824				
Thr Ser Tyr Pro Asn	Pro Ala Arg Val Glu	Ala Ala Tyr His Ile Leu					
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Glu Ala Leu Gln							
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 35 40 45
 Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu
 50 55 60
 Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr
 65 70 75 80
 Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys
 85 90 95
 Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys
 115 120 125
 Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln
 130 135 140
 Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
 145 150 155 160
 Cys Arg Ala Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu
 165 170 175
 His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
 180 185 190
 Arg Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 195 200 205
 Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu
 210 215 220

Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Pro Thr
 225 230 235 240
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Pro Val Ser Glu
 245 250 255
 Lys Gln Leu Ala Glu Val Val Ala Asn Thr Ile Thr Pro Leu Met Lys
 260 265 270
 Ala Gln Ser Val Pro Gly Met Ala Val Ala Val Ile Tyr Gln Gly Lys
 275 280 285
 Pro His Tyr Tyr Thr Phe Gly Lys Ala Asp Ile Ala Ala Asn Lys Pro
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 Val Thr Pro Gln Thr Leu Phe Glu Leu Gly Ser Ile Ser Lys Thr Phe
 305 310 315 320
 Thr Gly Val Leu Gly Gly Asp Ala Ile Ala Arg Gly Glu Ile Ser Leu
 325 330 335
 Asp Asp Ala Val Thr Arg Tyr Trp Pro Gln Leu Thr Gly Lys Gln Trp
 340 345 350
 Gln Gly Ile Arg Met Leu Asp Leu Ala Thr Tyr Thr Ala Gly Gly Leu
 355 360 365
 Pro Leu Gln Val Pro Asp Glu Val Thr Asp Asn Ala Ser Leu Leu Arg
 370 375 380
 Phe Tyr Gln Asn Trp Gln Pro Gln Trp Lys Pro Gly Thr Thr Arg Leu
 385 390 395 400
 Tyr Ala Asn Ala Ser Ile Gly Leu Phe Gly Ala Leu Ala Val Lys Pro
 405 410 415
 Ser Gly Met Pro Tyr Glu Gln Ala Met Thr Thr Arg Val Leu Lys Pro
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 Leu Lys Leu Asp His Thr Trp Ile Asn Val Pro Lys Ala Glu Glu Ala
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 His Tyr Ala Trp Gly Tyr Arg Asp Gly Lys Ala Val Arg Val Ser Pro
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 Gly Met Leu Asp Ala Gln Ala Tyr Gly Val Lys Thr Asn Val Gln Asp
 465 470 475 480
 Met Ala Asn Trp Val Met Ala Asn Met Ala Pro Glu Asn Val Ala Asp
 485 490 495
 Ala Ser Leu Lys Gln Gly Ile Ala Leu Ala Gln Ser Arg Tyr Trp Arg
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 Ile Gly Ser Met Tyr Gln Gly Leu Gly Trp Glu Met Leu Asn Trp Pro
 515 520 525
 Val Glu Ala Asn Thr Val Val Glu Thr Ser Phe Gly Asn Val Ala Leu
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Ala Pro Leu Pro Val Ala Glu Val Asn Pro Pro Ala Pro Pro Val Lys
545 550 555 560

Ala Ser Trp Val His Lys Thr Gly Ser Thr Gly Gly Phe Gly Ser Tyr
565 570 575

Val Ala Phe Ile Pro Glu Lys Gln Ile Gly Ile Val Met Leu Ala Asn
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<210> 5
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<210> 6
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<220>
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<210> 15
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<213> Artificial

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<223> Description of Artificial Sequence: Primer

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<210> 21

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<210> 22

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<212> PRT

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<400> 23

Met His Gly Thr Lys Leu

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5